

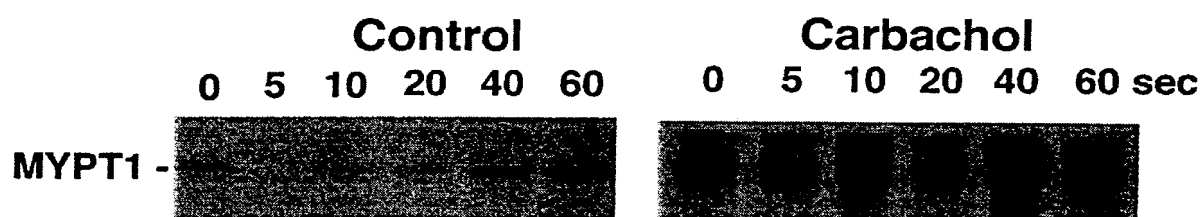
[illegible]

Figure 1B

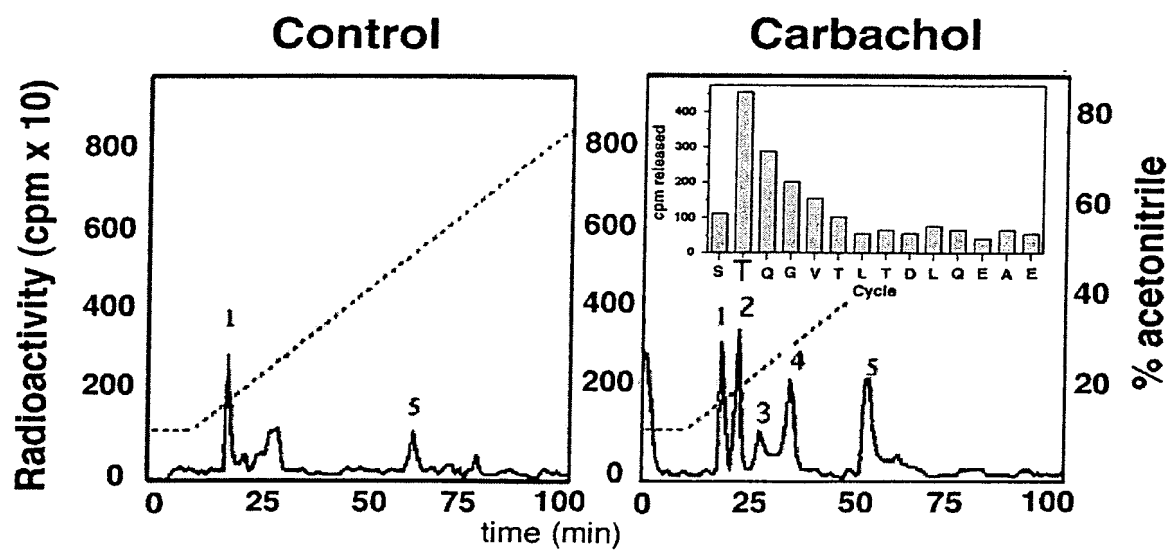


Figure 2A

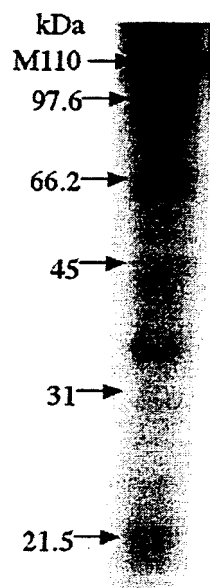


Figure 2B

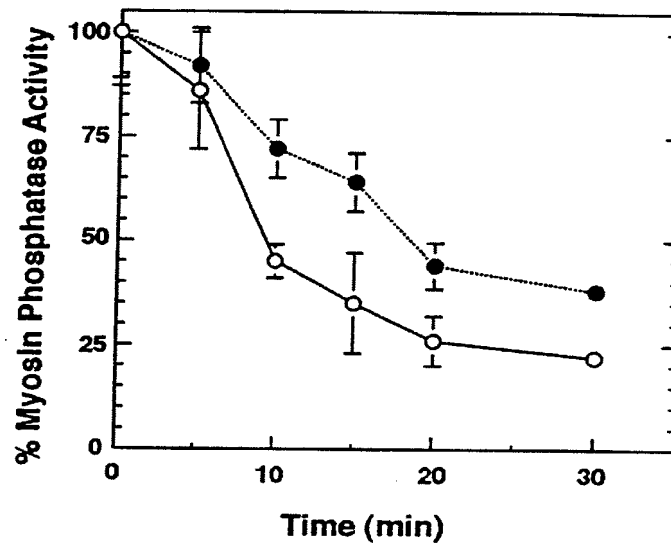
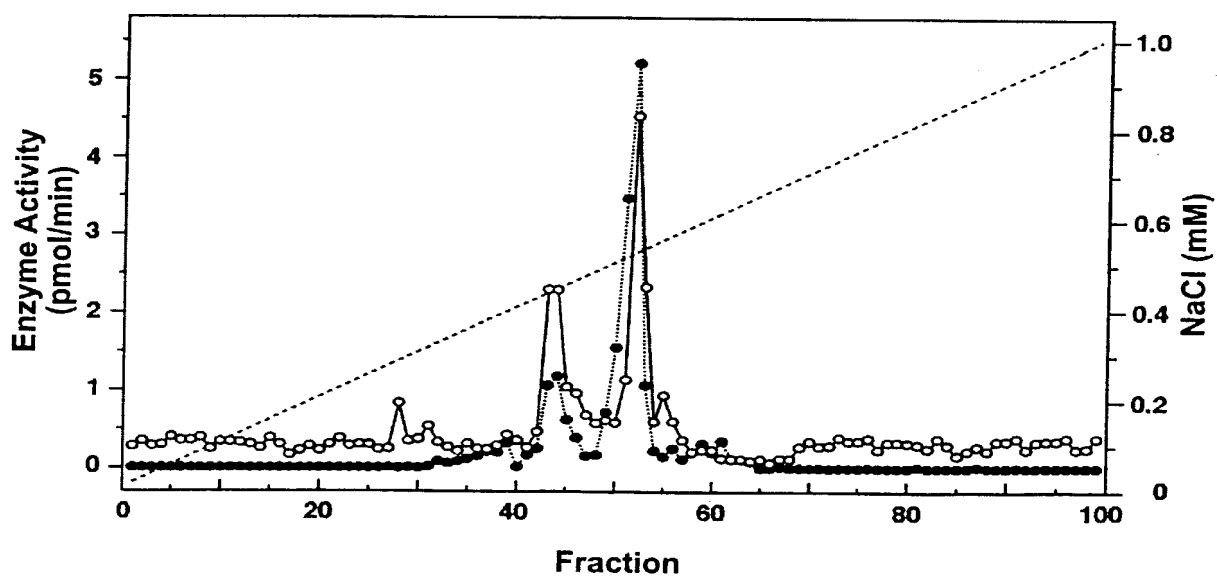
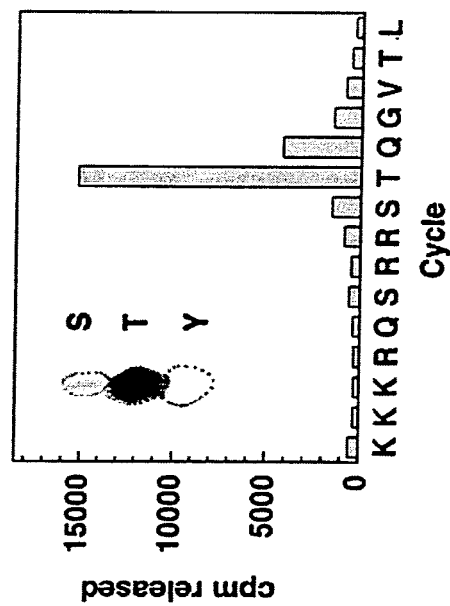
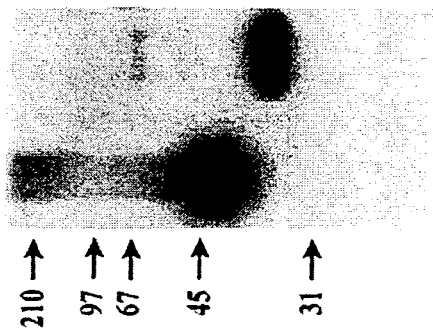
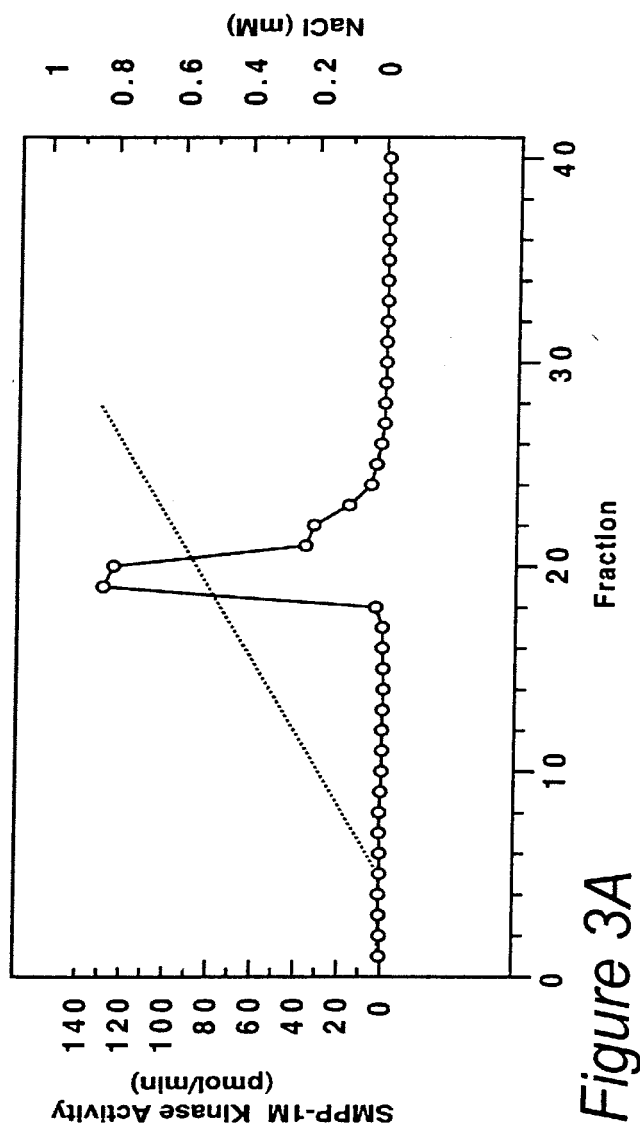


Figure 2





Edman cycle number	Amino acids recovered at each cycle	FASTF Aligned Sequence	Called Protein
1.	M M M M	MGEELGSGQFAIV-----	ZIP kinase
2.	D G T L	
3.	E I L V	MSTFRQEDVEDHYEMGEELGSGQFAIVRKCRCQKGTGKEYAAKFIKKRRLPSSRRGVSRREEIEREVNILREIRHPNIITLH	
4.	A T D E	10 20 30 40 50 60 70 80	
5.	Q K L X	-----	
6.	N R G X	-----MLLDKXIFXRPIQ--	
7.	I S L X	
8.	Y F G X	
9.	Q Y L X	DIFENKTDVVLILELVSGGELDFLAEKESLTFDEATQFLKQILDGVHYLHSKRIAHDLPENIMLLDKNVNPNRIKLI	
10.	R K F X	90 100 110 120 130 140 150 160	
11.	A P T X	-----	
12.	I T G I	-----	
	V E Q X	-----	
		DFGIAHKIEAGNEFKNIFGTPEFVAPEIVNVEPLGLEADMWSIGVITYILLSGASPFLGETKQETLTNISAVNYDFDEEY	
		170 180 190 200 210 220 230 240	
		-----MTIAQNLYXXIX-----	
		
		FSSTSELAKDFIRLLVKDPKRRMTIAQSLEHSWIKVRRREDGARKPERRRLRAARLREYSLKSHSSMPRNTSYASFERR	
		250 260 270 280 290 300 310 320	

Figure 4

Figure 5A

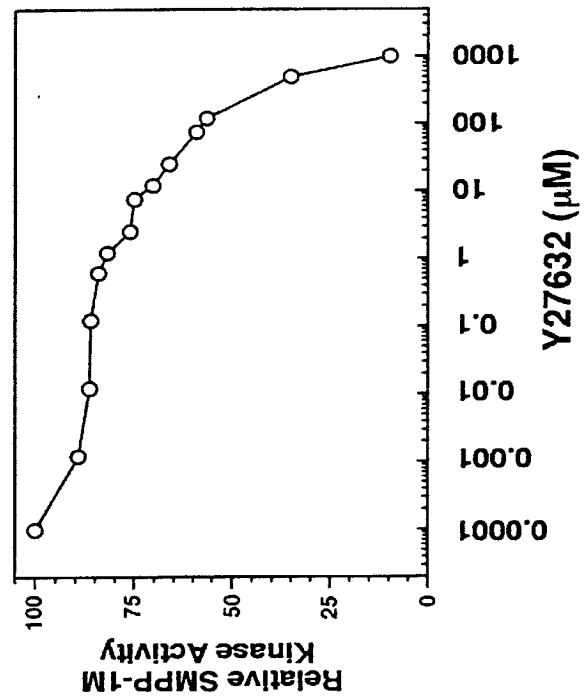


Figure 5B

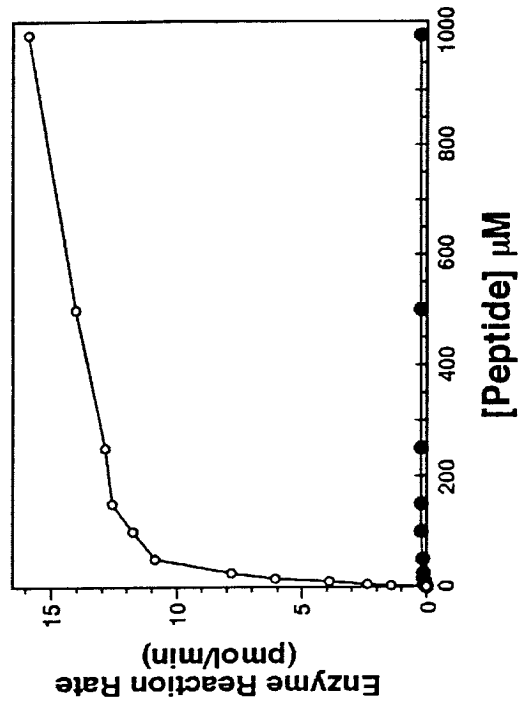


Figure 5C

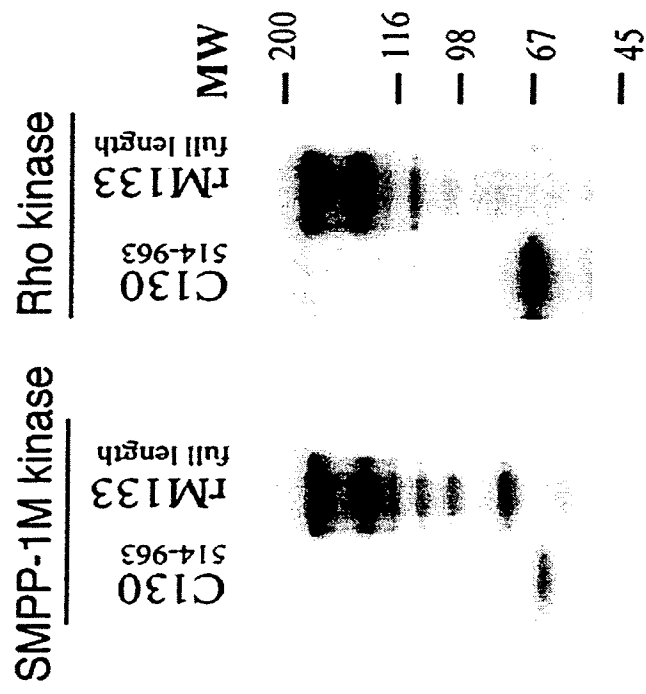


Figure 5D

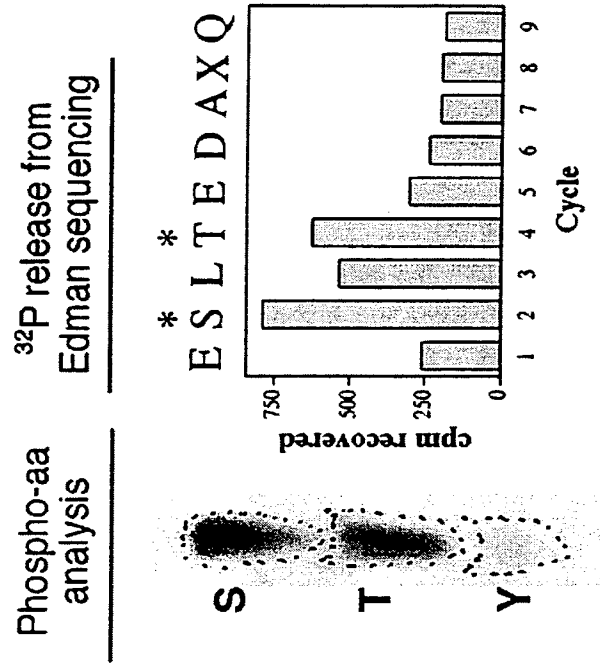


Figure 6E

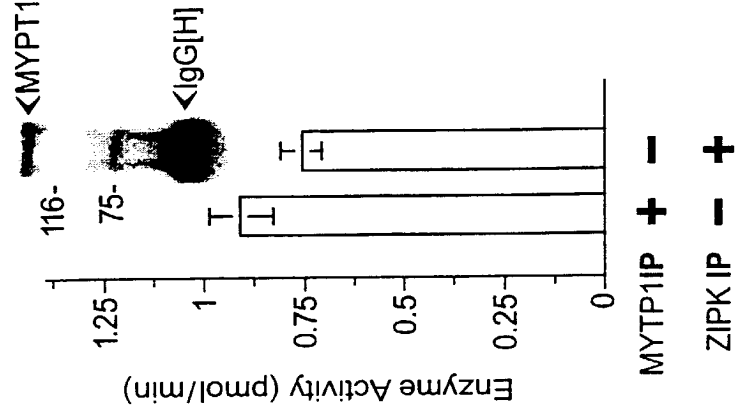


Figure 6D

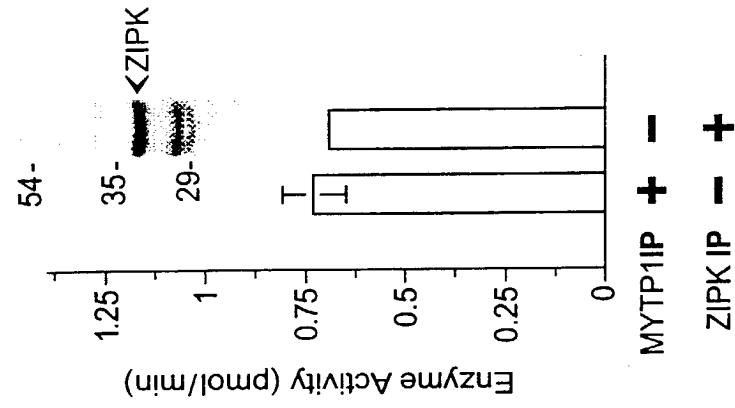


Figure 6A

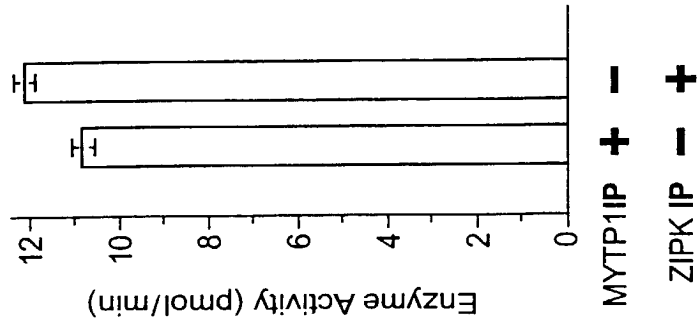


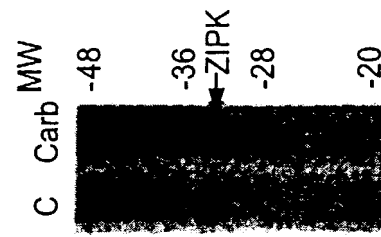
Figure 6C

Figure 6B

Figure 6A

Figure 1 is a line graph showing the fractionation of SMPP-1M Kinase Activity. The y-axis represents SMPP-1M Kinase Activity in pmol/min, ranging from 0 to 800. The x-axis represents the Fraction number, ranging from 0 to 40. Two data series are plotted: C (Control, open circles) and T (Treated, filled circles). Both series show a peak activity around fraction 15-20. A dotted line indicates a linear gradient across the fractions.

Fraction	C (pmol/min)	T (pmol/min)
0	0	0
5	100	100
10	250	250
15	400	400
20	550	550
25	600	600
30	650	650
35	700	700
40	750	750



Treatment	Relative SMPP-1M / ZIP-Kinase Activity (approx.)
Control	100
Carbachol (+)	130
Calyculin A (+)	115
Y-27632 (-)	155
Carbachol (+)	130
Calyculin A (-)	115
Y-27632 (-)	155
Carbachol (+)	130
Calyculin A (+)	115
Y-27632 (-)	155
Carbachol (-)	130
Calyculin A (+)	115
Y-27632 (+)	115

Figure 7C

Figure 8

Putative nucleotide sequence of smooth muscle MYPT-kinase showing start site in bold.

GNT AT GNATA	TCGGTTTAAT	CGGCCGGAGC	TCGCCCNCNG	GGCAGCTGGA	
CTCCCTCTCA	GACCTCCTTC	TTTCTCGCCC	TCAGCACGGG	ATTAACCTCA	100
CTTGACTGTT	CTTGGGTCCC	CGGTGCCGGG	CCAGCGTCCT	CTCCCTCAAG	150
GCAATCCCCA	AGTGTCTGTC	ATGAGGCTCT	TTGGGCAGTT	CTGTTGTTGT	200
GGGAAACCTG	GGAACAGATG	CACAGAGGCT	GGGGTACAGA	GTCCTGCCTT	250
CCTCTGGGTC	TGCAGCGCTT	AGCTGTTTCT	TCCCCACAG	CGGCCAGTTC	300
GCCATCGTGC	GCAAGTGCCA	GCAGAAGGGC	ACCGGCATGG	AGTACGCGGC	350
CAAGTTCATA	AAGAAGCGGC	GCCTGCCGTC	CAGCCGGCGC	GGTGTGAGCC	400
GTGAGGAGAT	CGAGCGCGAG	GTGAGCATCC	TGCGCGAGAT	CCGCCACCCC	450
AACATCATCA	CGCTGCACGA	TGTGTTTCGAG	AACAAGACAG	ATGTGGTGCT	500
GATCTTGGAG	CTGGTGTCCG	GCGGCGAACT	TTTCGACTTT	CTGGCTGAGA	550
AGGATCACTG	ACAGAGGATG	AGGCCACGCA	GTTCTCAAG	CAGATCCTGG	600
ACGGTGTCCA	CTACCTGCAC	TCCAAGCGCA	TCGCGCACTT	TGACCTGAAG	650
CCGGAGAACA	TCATGTTGCT	GGACAAGCAT	GCAGCCAGCC	CACGCATTAA	700
GCTCATCGAC	TTTGGCATCG	CGCACAGGAT	CGAGGCCGGT	AGCGAGTTCA	750
AGAACATCTT	TGGCACGCCA	GAGTTCGTCG	GTGAGGGGCA	GGTGTGGGCA	800
CCACCCGATA	GGGTAGATTT	TGCACGGCCT	TGGCCTGACC	TGCCTCAACA	850
ATCCTGTCTT	CCACAGCCCC	TGAGATTGTA	AACATGAAC	CACTTGCTT	900
GGAAGCTGAT	ATGTGGAGCA	TCGGCGTCAT	CACCTACATC	CTGTGAGTGC	950
CTGAGATGGG	CAGGGGCCTC	AGACTGTACC	TGCTAGAGGC	CCAGGGATCA	1000
GGGCTGGCAC	CTCTGCAAAC	TGCAAACACT	GGGGCTGAGA	GATGTCCCTG	1050
GGAACNCTGG	ATATGCCTGG	GCCCCACCAA	NGTAGGACCA	TNC	1093

Figure 9

Deduced amino acid sequence of rat aorta smooth muscle MYPT-kinase (underlined shows alignment with 52kDa ZIP kinase sequence)

MXI GL IGRS	SPXGQ LD SLS	DLLLSRPQHG	INLT*LFLGP	RCRASVLSLK
AIPK CL S*GS	LGSSVVVGNL	GTDAQRLGYR	VLPSSGSAAL	SCSFPHSGQF
<u>AIVRKCOOKG</u>	<u>TGMEYAAKEI</u>	<u>KKRRLPSSRR</u>	<u>GVSREEIERE</u>	<u>VSILREIRHP</u>
<u>NIITLHDVFE</u>	<u>NKTDVVLILE</u>	<u>LVSGGELEDF</u>	<u>LAEKDH*QRM</u>	<u>RPRSSSSRSW</u>
TVSTTCTPSA	SRTL T *SRRT	SCCWTSMPQA	HALSSSTLAS	RTGSRPVASS
RTSLARQSSS	VRGRCGHHPI	G*ILHGLGLT	CLNNPVFHSP	*DCKL*TTWL
GS*YVEHRRH	HLHPVSA*DG	QGPQTVPARG	PGIRAGTSAN	CKHWG*EMSL
GTLDMPGPHQ	XRTX			